sequence in SEQ ID NO: 1)) or 316 amino acid residues (murine, cf. SEQ ID NOs: 4 and 6 (corresponding DNA sequences in SEQ ID NOS: 3 and 5, respectively)). Alignment of the two amino acid sequences show that identical amino acid residues are found at 87% of the homologous positions.--

a1 cont

Please replace the paragraph beginning on page 24, line 20, with the following rewritten paragraph:

--The promiscuous epitope can according to the invention be a naturally occurring human T-cell epitope such as epitopes from tetanus toxoid (e.g. the P2 and P30 epitopes (SEQ ID NOS: 34 and 35, respectively)), diphtheria toxoid, Influenza virus hemagluttinin (HA), and *P. falciparum* CS antigen.--

a2

Please replace the paragraph beginning on page 25, line 31, with the following rewritten paragraph:

--One especially preferred PADRE peptide is the one having the amino acid sequence AKFVAAWTLKAAA (SEQ ID NO: 36) or an immunologically effective subsequence thereof. This, and other epitopes having the same lack of MHC restriction are preferred T-cell epitopes which should be present in the OPGL analogues used in the inventive method. Such super-promiscuous epitopes will allow for the most simple embodiments of the invention wherein only one single modified OPGL is presented to the vaccinated animal's immune system.--

a3

Please replace the paragraph beginning on page 54, line 18, with the following rewritten paragraph:

--A synthetic cDNA encoding the murine OPGL residues 158-316 has been synthesized removing sub-optimal *Eschericia coli* and *Pichia pastoris* codons from the published sequence. Additionally, an N-terminal Histidine tag, part of the cleavage site of the alpha mating factor signal sequence from *Sacharomyces cerevisiae*, and suitable restriction enzymes have been incorporated into the open reading frame (cf. SEQ ID NO: 7 (corresponding amino acid sequence in SEQ ID NO: 8)).--

a4

Please replace the paragraph beginning on page 54, line 25, with the following rewritten paragraph:

--This cDNA encoding wild type murine OPGL has been cloned into a standard *Eschericia coli* expression vector (pTrc99a) using *Bsp*HI and *Hind*III restriction enzymes and a standard cloning vector (pBluescript KS+) using *Sac*I and *Kpn*I restriction enzymes (yielding SEQ ID NO: 9 (corresponding amino acid sequence in SEQ ID NO: 10)).--

a5

Please replace the paragraph beginning on page 58, line 5, with the following rewritten paragraph:

--PCR of SEQ ID NO: 9 was performed using SEQ ID NOs: 22 and 25 as primers. The resulting PCR fragment was restriction digested with *Sac*II and *Kpn*I and subsequently purified from an agarose gel. A second PCR using SEQ ID NO: 9 as template was performed using primer SEQ ID NO: 26 and a vector specific primer. The resulting PCR fragment was restriction digested with *Kpn*I and *Hind*III. Both

a6

fragments were then ligated to SEQ ID NO: 9 in pBluescript KS+ restriction digested with *Sac*II and *Hind*III. To correct a single base mutation in this construct, PCR using the construct as template was performed with primers SEQ ID NOs: 33 and 29. The resulting PCR fragment was restriction digested with *Pst*I + *Eco*RI, gel purified and subsequently ligated to the erroneous construct digested with *Pst*I and *Eco*RI. The verified construct (SEQ ID NO: 13 (corresponding amino acid sequence in SEQ ID NO: 14)) was then transferred to pTrc99a using *Bsp*HI and *Hind*III restriction enzymes.--

a6 cont

Please replace the paragraph beginning on page 58, line 23, with the following rewritten paragraph:

--PCR was performed using primers SEQ ID NOs: 27 and 28 without template. The resulting PCR fragment was restriction digested with *Pst*I and *Eco*RI and subsequently purified from an agarose gel. The resulting fragment was then ligated to SEQ ID NO: 9 in pBluescript KS+ restriction digested with *Sac*II and *Hind*III. The verified construct (SEQ ID NO: 15 (corresponding amino acid sequence in SEQ ID NO: 16)) was subsequently transferred to pTrc99a using *Bsp*HI and *Hind*III restriction enzymes.--

a7

Please replace the paragraph beginning on page 59, line 1, with the following rewritten paragraph:

--PCR of SEQ ID NO: 9 was performed using primers SEQ ID NOs: 22 and 29. The resulting PCR fragment was restriction digested with *Pst*I and *Bst*BI and subsequently purified from an agarose gel. A second PCR using SEQ ID NO: 9 as template was performed using primer SEQ ID NO: 30 and a vector specific primer. The resulting PCR fragment was

a8

restriction digested with *Bst*BI and *Kpn*I and subsequently gel purified. Both fragments were then ligated to SEQ ID NO: 9 in pBluescript KS+ restriction digested with *Pst*I and *Kpn*I. The verified construct (SEQ ID NO: 17 (corresponding amino acid sequence in SEQ ID NO: 18)) was then transferred to pTrc99a using *Bsp*HI and *Hind*III restriction enzymes.

a8 Cont

Please replace the paragraph beginning on page 59, line 14, with the following rewritten paragraph:

PCR of SEQ ID NO: 9 was performed using primers SEQ ID NOs: 22 and 23. The resulting PCR fragment was restriction digested with *Sac*II and *Kpn*I and subsequently purified from an agarose gel. A second PCR using SEQ ID NO: 9 as template was performed using primer SEQ ID NOs: 24 and 31. The PCR fragment was restriction digested with *Kpn*I and *Eco*RI and subsequently gel purified. Both fragments were then ligated to SEQ ID NO: 9 in pBluescript KS+ restriction digested with *Sac*II and *Eco*RI. The verified construct (SEQ ID NO: 19 (corresponding amino acid sequence in SEQ ID NO: 20)) was then transferred to pTrc99a using *Bsp*HI and *Hind*III restriction enzymes.

a9

Please delete pages 1-32 of the Sequence Listing originally filed on March 14, 2001 located immediately after the claims. Please insert the Substitute Sequence Listing enclosed herewith immediately after the claims.